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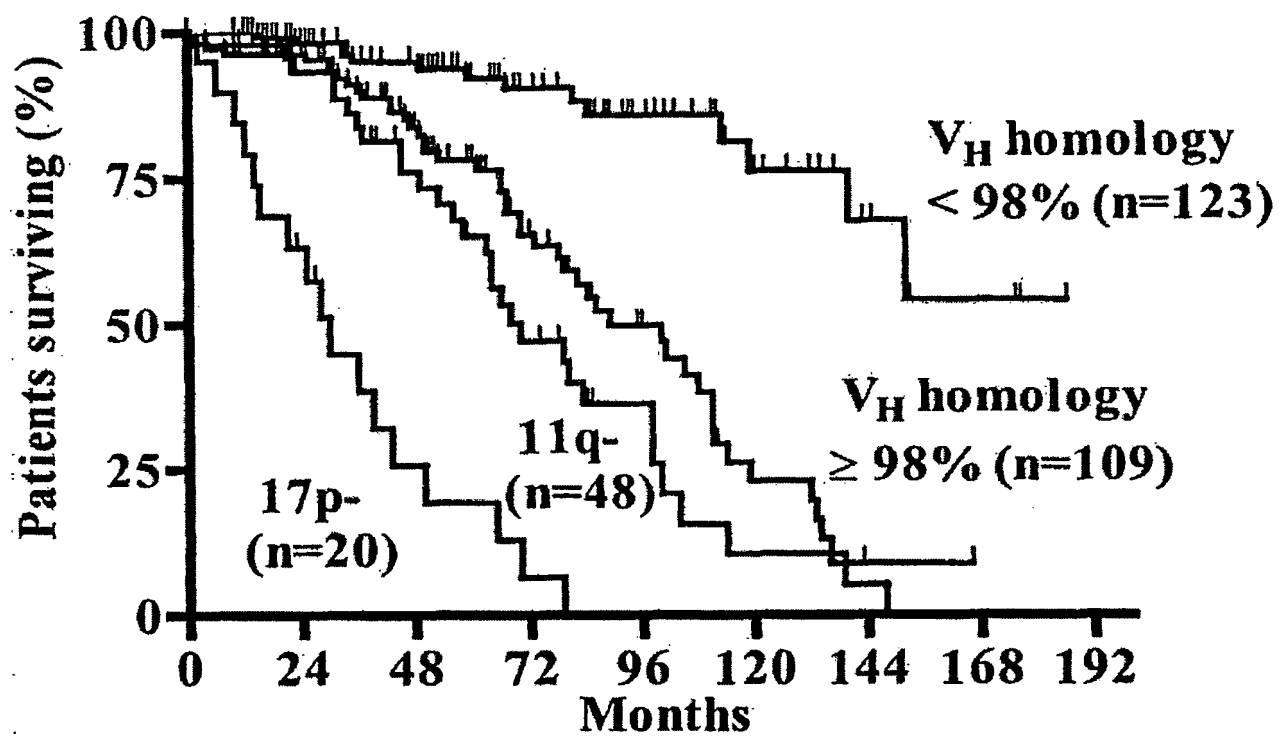


Fig. 1

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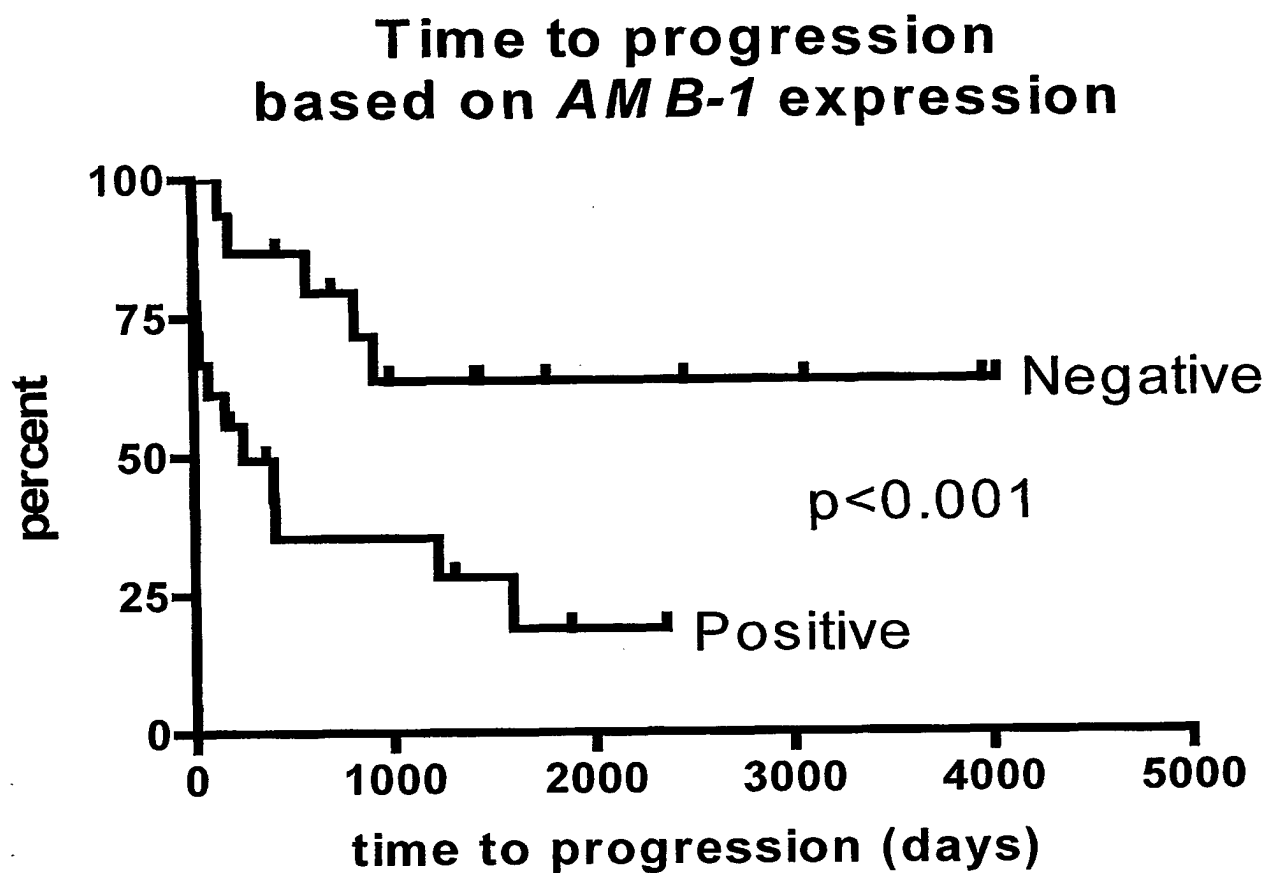


Fig. 2a

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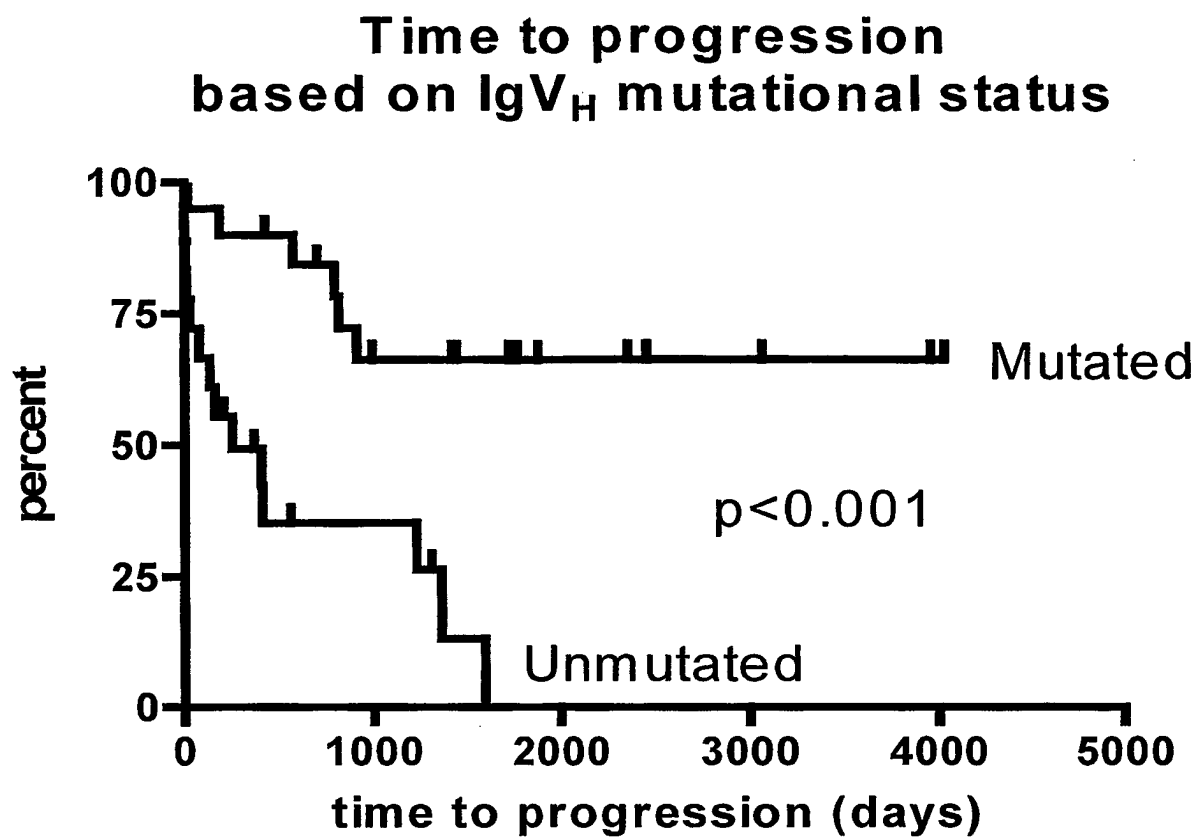


Fig. 2b

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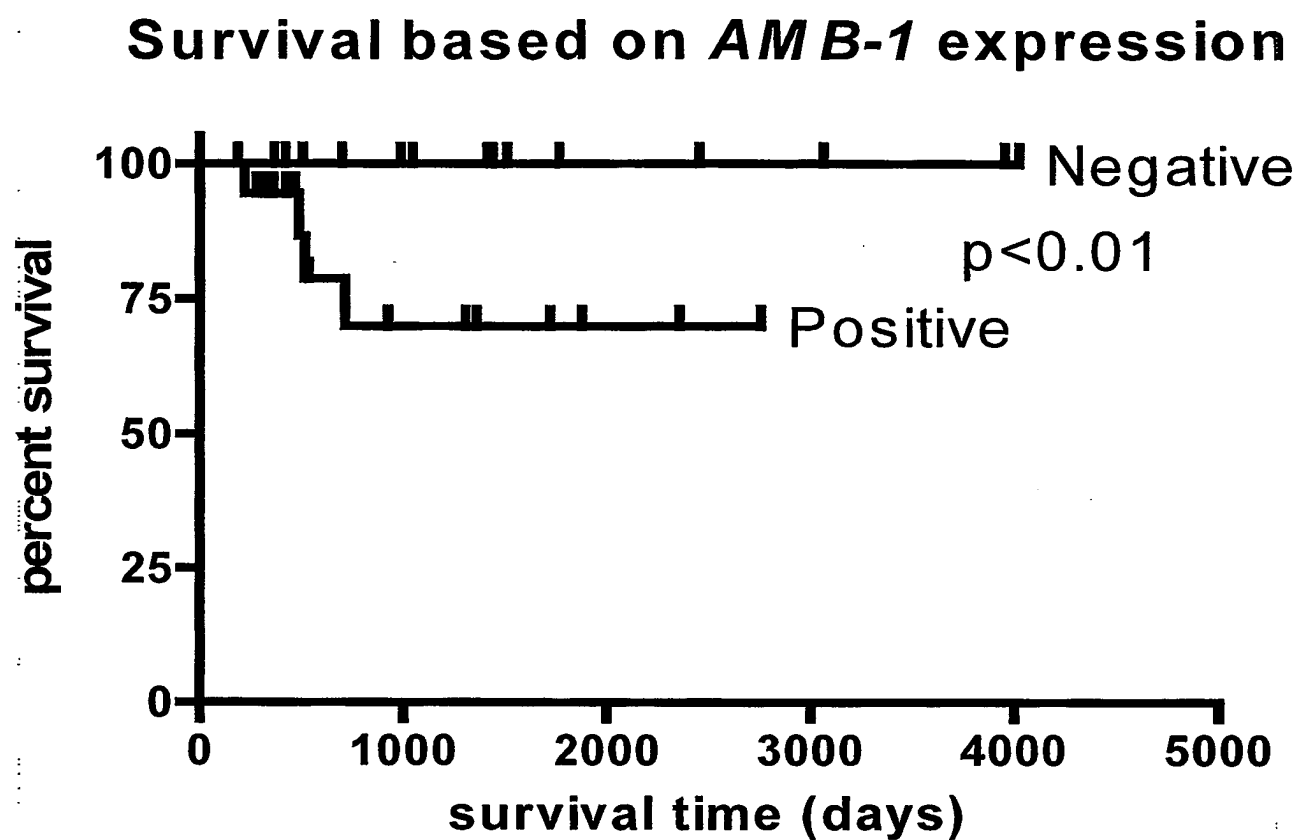


Fig. 2c

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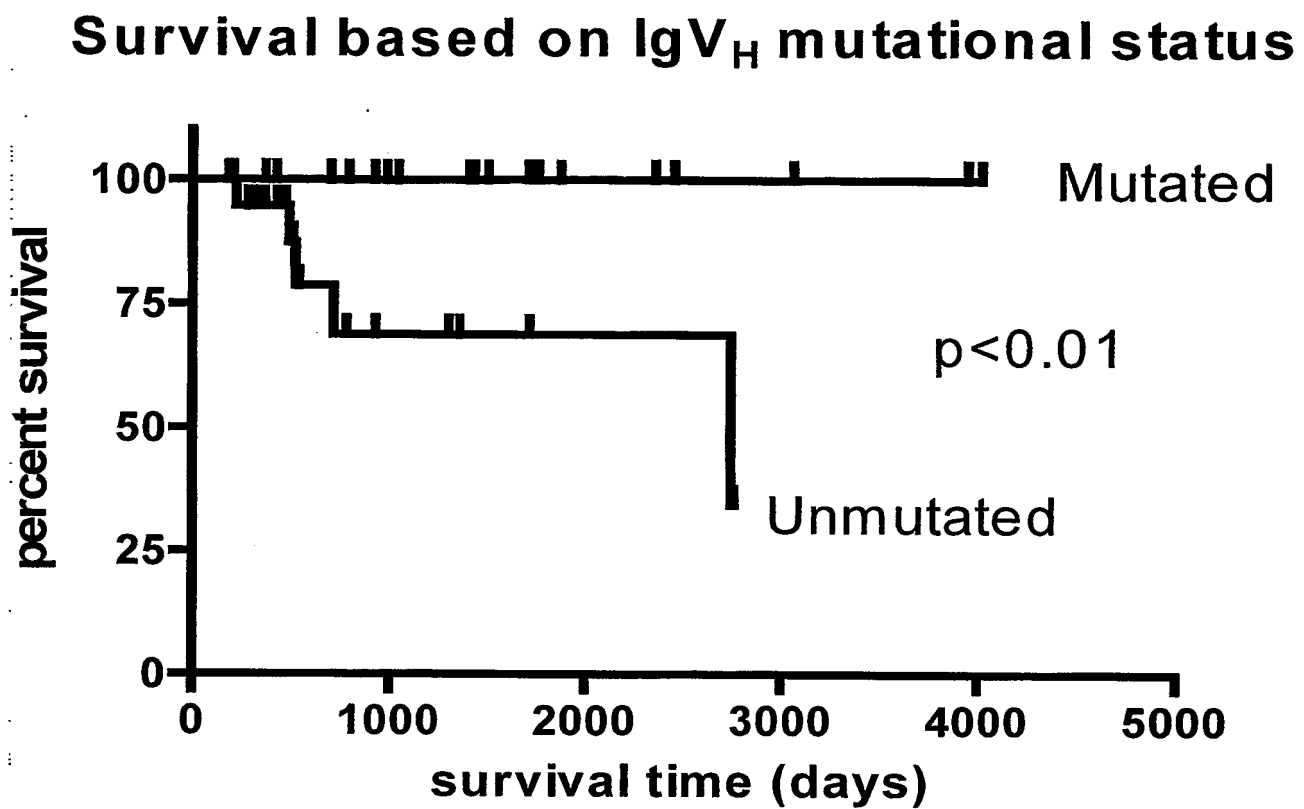


Fig. 2d

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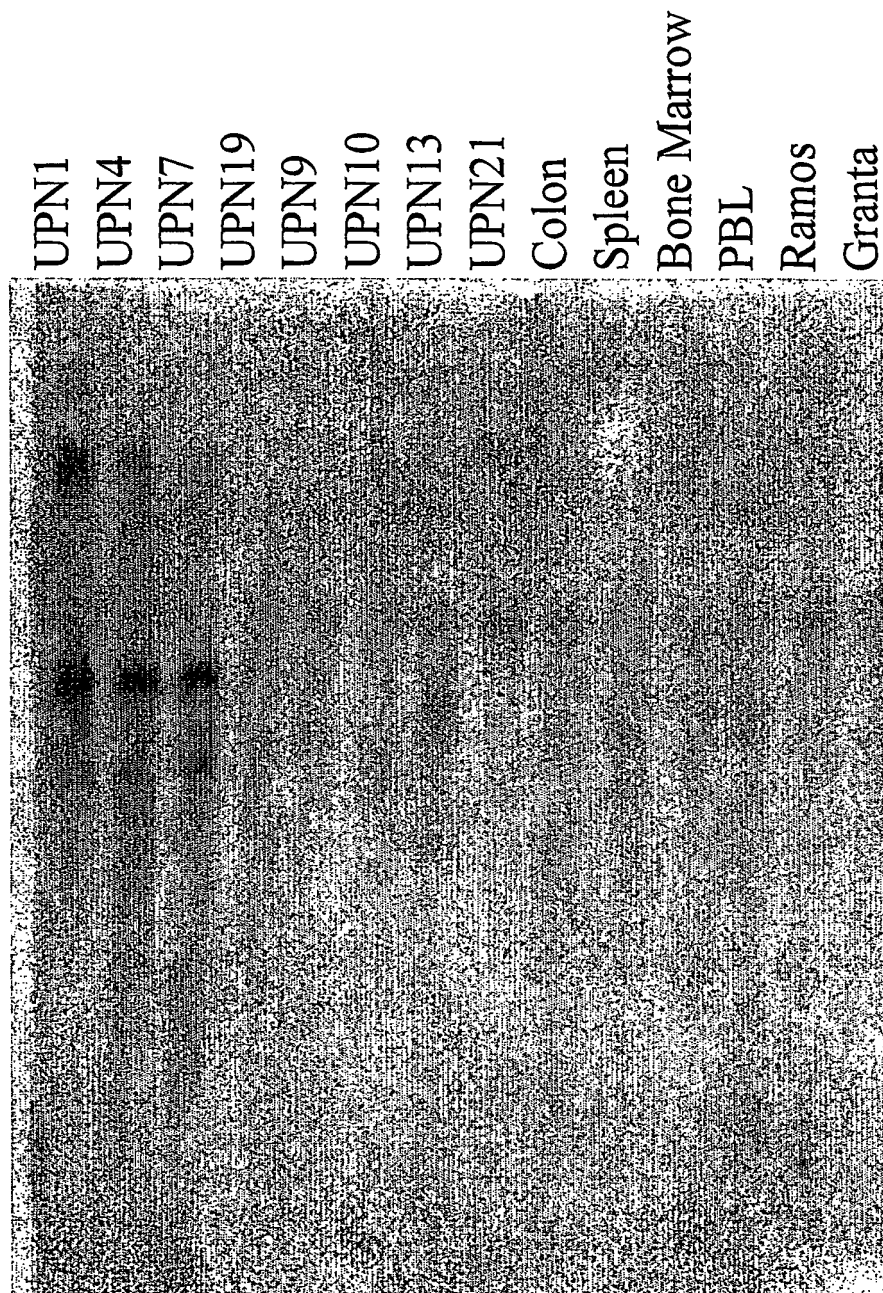


Fig. 3

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AMB1_pe_pSS	CCCCCCCCC	CCCCCCCCC	HHHHHHHHH	HHHEEECCC	CCCCEEEE
AMB1_pe_seq	MFNKCSFHSS	TYRPAADNSA	SSLCAIICFL	NLVI ECDLET	NS EINKLIY
-----			-+L--II--L	N--+	+-- +L-+-
dliara_seq		HKCD	ITLQEIIKTL	NSL	KTLC TELTVT
dliara_SS		CCCC	HHHHHHHHH	HHH	CCCCCCCC
CORE		0000	0010040015	005	0000100041
AMB1_pe_pSS	EECCCCCCH	HHHHHHHHH	HH HHCCHH	HHH	HHHH
AMB1_pe_seq	LFSQNNRIR	FSKLLKILF	YI SIFSYPE	LMC	EQYV
-----	+F+--+	-+-+---	+S+-E	--C	+Q-+
dliara_seq	DIFAASKNTT	EKETFCRAAT	VL RQFYSHHE	KDTRCLGATA	QQFHRHKQLI
dliara_SS	CCCCCCCCC	HHHHHHHHH	HHHHHHHHH	CCHHCCCCCH	HHHHHHHHH
CORE	0430000000	0001200920	4900300000	0000000000	0000000030
AMB1_pe_pSS	HHHC	CCCCCCC	CCCC	HHH	CCCCCE
AMB1_pe_seq	TFIK	PGIHYGQ	VSKKH	TFL	SKNFKF
-----	-F+K	-G+---	V++	FL	SK--
dliara_seq	RFLKRLDRNL	WGLAGLNSCP	VKEANQSTLE	NFLERLKTIM	REKYSKCSS
dliara_SS	HHHHHHHHH	HHHCCCCC	CCCCCEEH	HHHHHHHHH	HHHHCCCC
CORE	0160080008	0011000000	2000002060	0560080013	0000000000
AMB1_pe_pSS	EEEEEC				
AMB1_pe_seq	QLLRVCW				

dliara_seq					
dliara_SS					
CORE					

Fig.4

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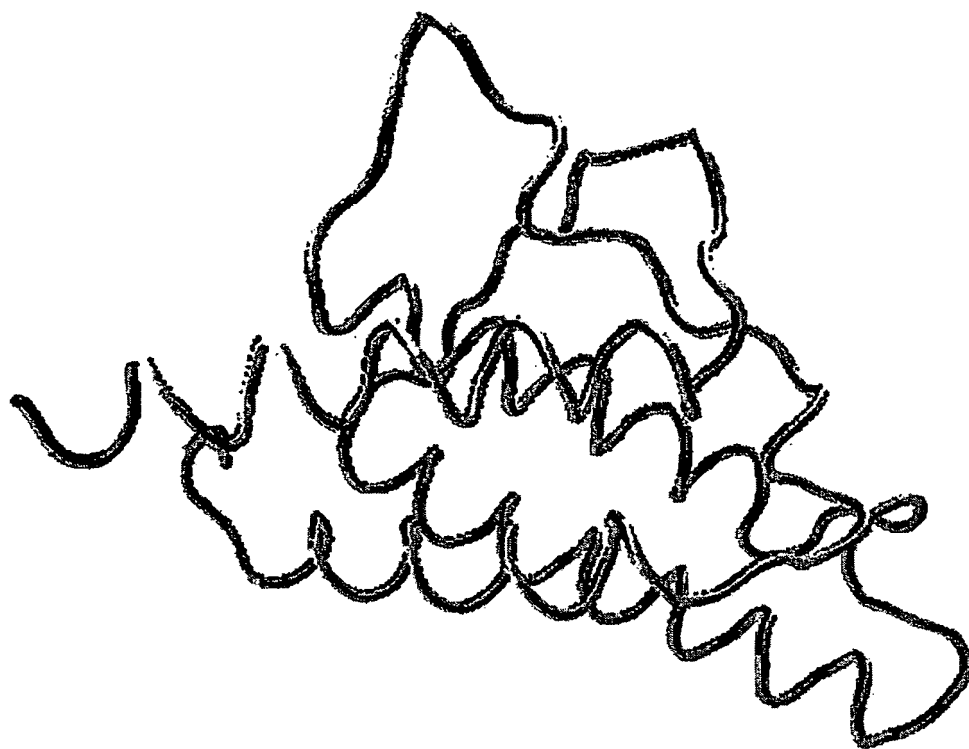
Seed Library	Template Length	Model	PSSM E-value	SAWATED E-value	BioText	Class	Fold	Superfamily	Family	Protein
d1p3212 25% i.d.	75		2.88	1	n/a	Alpha and beta proteins (ab)	Thioredoxin fold	Thioredoxin-like	Glutathione S-transferases, N-terminal domain	Glutathione S-transferase
d1iaa 17% i.d.	129		3.05	1	n/a	All alpha proteins	4-helical cytokines	4-helical cytokines	Short-chain cytokines	Interleukin-4 (IL-4)
c1dga 17% i.d.	89		5.34	1	n/a	not in SCOP 1.53	PDB header: hydrolase inhibitor.	Chain A: PDB Molecule: berg (protease inhibitor).		PDBTitle: solution structure of interleukin-2 1beta generation.
d1am3a 22% i.d.	80		5.57	1	n/a	All alpha proteins	Helix-loop-helix DNA-binding domain	Helix-loop-helix DNA-binding domain	Helix-loop-helix DNA-binding domain	SREBP-1a

Fig.5

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Human IL4



AMB1

Fig.6

AMB1 IL4 IL3 IL13 GA-CSF

-----MENKCSFHSSYRRPADNSASSLCALICE-----LNLVIECDLE--TNS--EINKLIY--LFSQNRIRFSKLLKILFYI--SIESYPE--LNC-----EQVYTFIK-----PGIHGVSKKH--IYIS--TFISKNTKFOILLRVCH
IL4 -----HKCDITIQELIKT-----INSL-----TE-QKT-ICTELTVDIEPASKNTTEKTCRAATVIAQFYSHKEDTRC--LGHATAQOFRHRKQILRETLRLDRNLWGL-----AGLNSCPVKEANOSTLE--NFIERLAKTIMREKYSKCS--
IL3 -----ANCSIMIDE--IIHH-----LARPENLLDEN-----NLAN--SEMDILMERNLRTNLLAFVRAVKHLENASYES-----ILKNLLPCPL-ATAAPTRPHPIKOG--DWNFE-----RRKLTFFYKLTLENAAQOQ
IL13 MALLITTVIALTCUGSFASPGVPPSTALRELIEE--LNNI-----TONOKAPLNGSSWWSI-----NLTA--GMYCALESILNV-----SGCSAIEK-----TQRMISGFCPH-KVSGQFSSLSLVRDTKIEVAQF-----VKOLLHLHKKLFREGREN
CSF -----RSPFSSTQPMHVNVAIQEARRLML-----SROTHADEMETVEVISEM-----FDLQE--PTCLQTRUELYRQ-----LKGPLTWASHYKQHCPPPTPETSATQIITFESF--KENLAKDFLLVIPEDCWEP

Fig. 7

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	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum right	accumbens nucleus	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia K-562	fetal kidney	<i>E.coli</i> rRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	<i>E.coli</i> DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	Poly r(A)
F	temporal lobe	hippocampus		ventricle right	ileocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human Cyt-1 DNA
G	p.g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adeno-carcinoma SW480	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma A549		human DNA 500 ng

Fig. 8

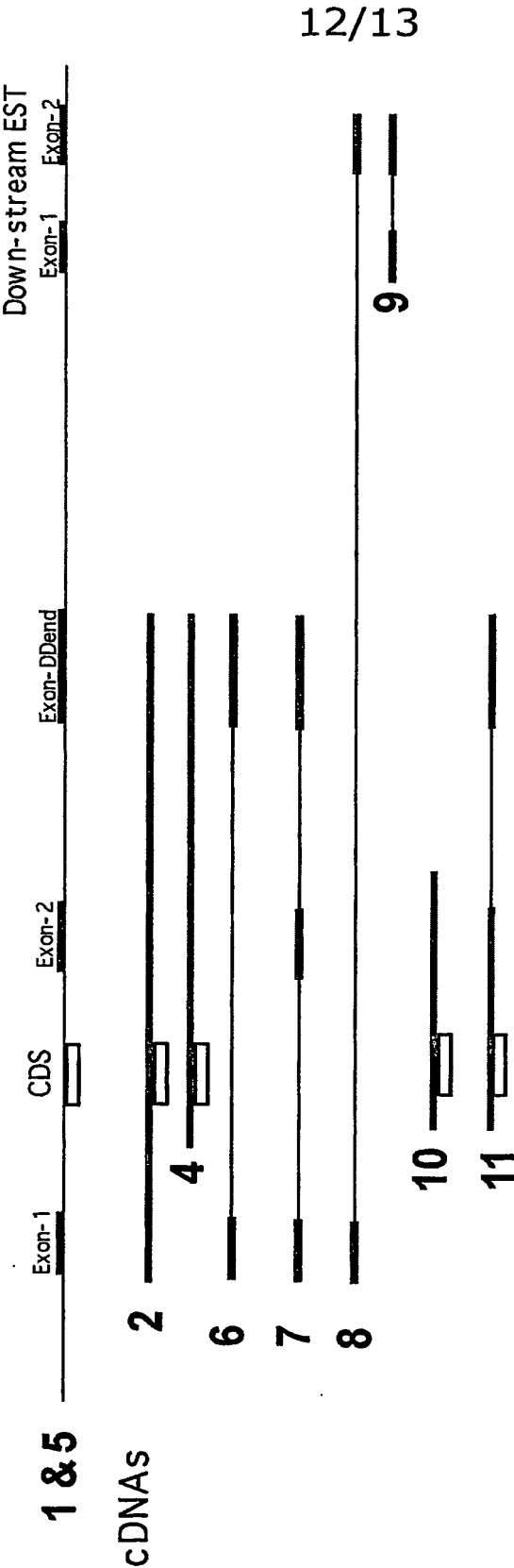


Fig. 9

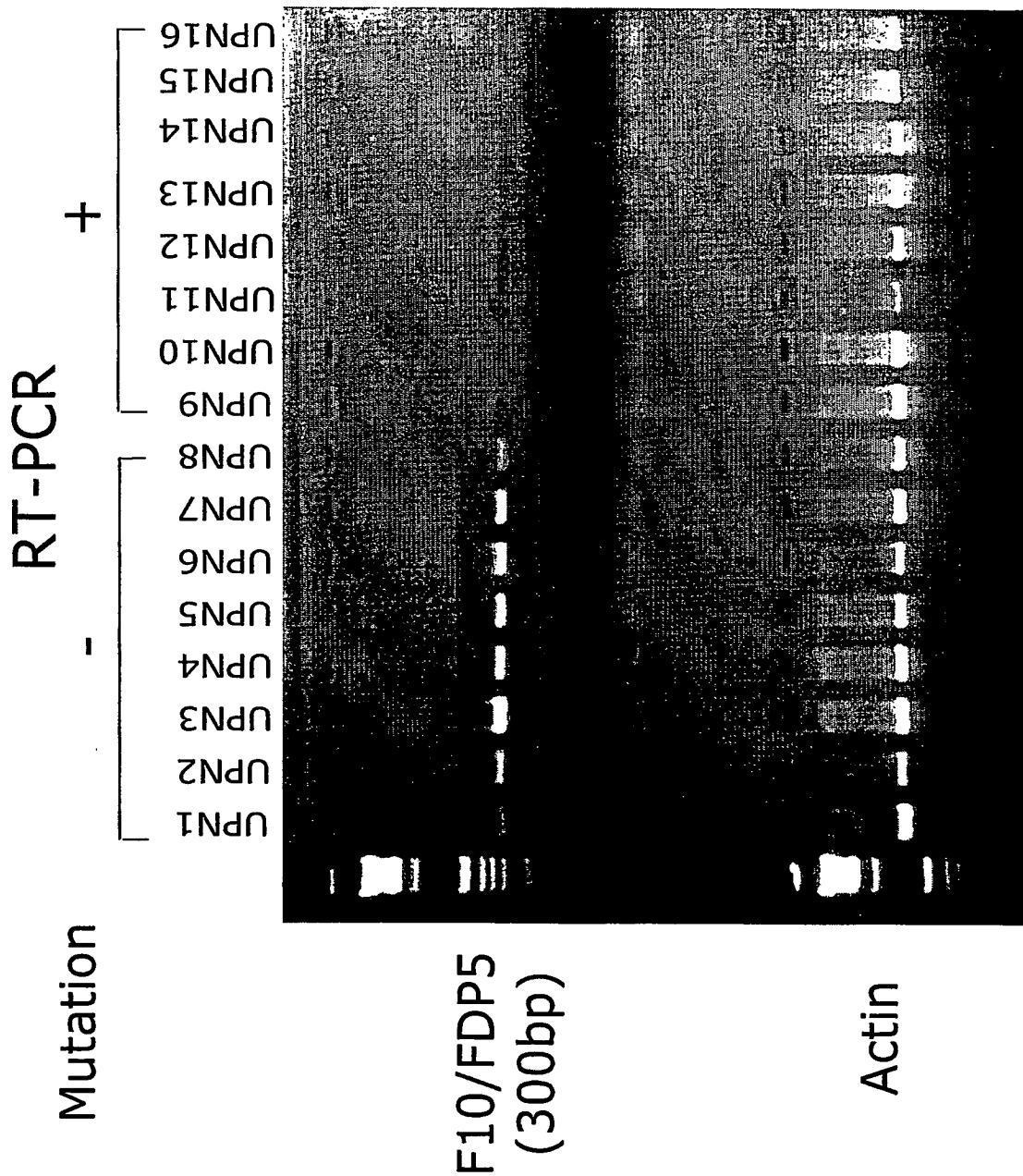


Fig. 10